

RAW SEQUENCE LISTING

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Application Serial Number: 101791, 853 B
Source: FWO
Date Processed by STIC: 4-21-05

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IFWO

RAW SEQUENCE LISTING

DATE: 04/21/2005

PATENT APPLICATION: US/10/791,853B

TIME: 11:41:24

Input Set : E:\OP1387seqUS.txt

Output Set: N:\CRF4\04212005\J791853B.raw

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3 <110> APPLICANT: TAKASHITA, Ryo
4   YASUEDA, Hisashi
5   GUNJI, Yoshiya
7 <120> TITLE OF INVENTION: METHOD FOR PRODUCING ALCOHOL BY USING MICROORGANISM
W--> 9 <130> FILE REFERENCE:
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/791,853B
C--> 11 <141> CURRENT FILING DATE: 2004-03-04
11 <150> PRIOR APPLICATION NUMBER: JP 2001-270903
12 <151> PRIOR FILING DATE: 2001-09-06
14 <160> NUMBER OF SEQ ID NOS: 5
16 <170> SOFTWARE: PatentIn Ver. 2.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 38
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
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45 <220> FEATURE:
46 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
48 <400> SEQUENCE: 3
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56 <220> FEATURE:
57 <223> OTHER INFORMATION: Description of Artificial Sequence:primer
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69 <222> LOCATION: (1478)..(3061)
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73 <222> LOCATION: (3142)..(4311)
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76 <221> NAME/KEY: CDS
77 <222> LOCATION: (4328)..(4753)
79 <220> FEATURE:
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81 <222> LOCATION: (4764)..(5276)
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94 gcttcctgca ggatgtcgat cttgttcaac accaaaaaga tacggccggc gtacttccgg 180
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103 gcgcagagcg gcggggaggc gtccgccagc tcgtcgatca ggctcaggag ttcggttttg 720
104 agatccgcag agccggtcgt tggcgccca ccggcgatcg gccaacgggg gatcgcggtc 780
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112 gttatggcgg ccagtagct caccgttatg tccgatggct gtatcaaaca aagacacgtg 1260
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115 taggttgtca cgacctcgtc ggaggttgta tgtccggtgt tccgtgacgt catcgggcat 1440
116 tcatcattca tagaatgtgt tacggaggaa acaagta atg gca ctt agc acc gca 1495
117                                     Met Ala Leu Ser Thr Ala

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118											1			5			
119	acc	aag	gcc	gcg	acg	gac	gcg	ctg	gct	gcc	aat	cgg	gca	ccc	acc	agc	1543
120	Thr	Lys	Ala	Ala	Thr	Asp	Ala	Leu	Ala	Ala	Asn	Arg	Ala	Pro	Thr	Ser	
121				10						15				20			
122	gtg	aat	gca	cag	gaa	gtg	cac	cgt	tgg	ctc	cag	agc	ttc	aac	tgg	gat	1591
123	Val	Asn	Ala	Gln	Glu	Val	His	Arg	Trp	Leu	Gln	Ser	Phe	Asn	Trp	Asp	
124			25				30					35					
125	ttc	aag	aac	aac	cgg	acc	aag	tac	gcc	acc	aag	tac	aag	atg	gcg	aac	1639
126	Phe	Lys	Asn	Asn	Arg	Thr	Lys	Tyr	Ala	Thr	Lys	Tyr	Lys	Met	Ala	Asn	
127		40					45					50					
128	gag	acc	aag	gaa	cag	ttc	aag	ctg	atc	gcc	aag	gaa	tat	gcg	cgc	atg	1687
129	Glu	Thr	Lys	Glu	Gln	Phe	Lys	Leu	Ile	Ala	Lys	Glu	Tyr	Ala	Arg	Met	
130	55					60				65					70		
131	gag	gca	gtc	aag	gac	gaa	agg	cag	ttc	ggg	agc	ctg	cag	gat	gcg	ctg	1735
132	Glu	Ala	Val	Lys	Asp	Glu	Arg	Gln	Phe	Gly	Ser	Leu	Gln	Asp	Ala	Leu	
133					75				80					85			
134	acc	cgc	ctc	aac	gcc	ggg	gtt	cgc	gtt	cat	ccg	aag	tgg	aac	gag	acc	1783
135	Thr	Arg	Leu	Asn	Ala	Gly	Val	Arg	Val	His	Pro	Lys	Trp	Asn	Glu	Thr	
136				90					95					100			
137	atg	aaa	gtg	gtt	tcg	aac	ttc	ctg	gaa	gtg	ggc	gaa	tac	aac	gcc	atc	1831
138	Met	Lys	Val	Val	Ser	Asn	Phe	Leu	Glu	Val	Gly	Glu	Tyr	Asn	Ala	Ile	
139			105					110					115				
140	gcc	gct	acc	ggg	atg	ctg	tgg	gat	tcc	gcc	cag	gcg	gcg	gaa	cag	aag	1879
141	Ala	Ala	Thr	Gly	Met	Leu	Trp	Asp	Ser	Ala	Gln	Ala	Ala	Glu	Gln	Lys	
142		120					125				130						
143	aac	ggc	tat	ctg	gcc	cag	gtg	ttg	gat	gaa	atc	cgc	cac	acc	cac	cag	1927
144	Asn	Gly	Tyr	Leu	Ala	Gln	Val	Leu	Asp	Glu	Ile	Arg	His	Thr	His	Gln	
145	135				140					145					150		
146	tgt	gcc	tac	gtc	aac	tac	tac	ttc	gcg	aag	aac	ggc	cag	gac	ccg	gcc	1975
147	Cys	Ala	Tyr	Val	Asn	Tyr	Tyr	Phe	Ala	Lys	Asn	Gly	Gln	Asp	Pro	Ala	
148					155				160					165			
149	ggg	cac	aac	gat	gct	cgc	cgc	acc	cgt	acc	atc	ggg	ccg	ctg	tgg	aag	2023
150	Gly	His	Asn	Asp	Ala	Arg	Arg	Thr	Arg	Thr	Ile	Gly	Pro	Leu	Trp	Lys	
151				170				175					180				
152	ggc	atg	aag	cgc	gtg	ttt	tcc	gac	ggc	ttc	att	tcc	ggc	gac	gcc	gtg	2071
153	Gly	Met	Lys	Arg	Val	Phe	Ser	Asp	Gly	Phe	Ile	Ser	Gly	Asp	Ala	Val	
154			185					190					195				
155	gaa	tgc	tcc	ctc	aac	ctg	cag	ctg	gtg	ggg	gag	gcc	tgc	ttc	acc	aat	2119
156	Glu	Cys	Ser	Leu	Asn	Leu	Gln	Leu	Val	Gly	Glu	Ala	Cys	Phe	Thr	Asn	
157		200					205				210						
158	ccg	ctg	atc	gtc	gca	gtg	acc	gaa	tgg	gct	gcc	gcc	aac	ggc	gat	gaa	2167
159	Pro	Leu	Ile	Val	Ala	Val	Thr	Glu	Trp	Ala	Ala	Ala	Asn	Gly	Asp	Glu	
160	215				220					225					230		
161	atc	acc	ccg	acg	gtg	ttc	ctg	tcg	atc	gag	acc	gac	gaa	ctg	cgc	cac	2215
162	Ile	Thr	Pro	Thr	Val	Phe	Leu	Ser	Ile	Glu	Thr	Asp	Glu	Leu	Arg	His	
163					235				240					245			
164	atg	gcc	aac	ggg	tac	cag	acc	gtc	gtt	tcc	atc	gcc	aac	gat	ccg	gct	2263
165	Met	Ala	Asn	Gly	Tyr	Gln	Thr	Val	Val	Ser	Ile	Ala	Asn	Asp	Pro	Ala	
166				250				255						260			

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167	tcc	gcc	aag	tat	ctc	aac	acg	gac	ctg	aac	aac	gcc	ttc	tgg	acc	cag	2311
168	Ser	Ala	Lys	Tyr	Leu	Asn	Thr	Asp	Leu	Asn	Asn	Ala	Phe	Trp	Thr	Gln	
169			265					270					275				
170	cag	aag	tac	ttc	acg	ccg	gtg	ttg	ggc	atg	ctg	ttc	gag	tat	ggc	tcc	2359
171	Gln	Lys	Tyr	Phe	Thr	Pro	Val	Leu	Gly	Met	Leu	Phe	Glu	Tyr	Gly	Ser	
172			280					285					290				
173	aag	ttc	aag	gtc	gag	ccg	tgg	gtc	aag	acg	tgg	gac	cgc	tgg	gtg	tac	2407
174	Lys	Phe	Lys	Val	Glu	Pro	Trp	Val	Lys	Thr	Trp	Asp	Arg	Trp	Val	Tyr	
175	295					300					305					310	
176	gag	gac	tgg	ggc	ggc	atc	tgg	atc	ggc	cgt	ctg	ggc	aag	tac	ggg	gtg	2455
177	Glu	Asp	Trp	Gly	Gly	Ile	Trp	Ile	Gly	Arg	Leu	Gly	Lys	Tyr	Gly	Val	
178				315						320					325		
179	gag	tcg	ccg	cgc	agc	ctc	aag	gac	gcc	aag	cag	gac	gct	tac	tgg	gct	2503
180	Glu	Ser	Pro	Arg	Ser	Leu	Lys	Asp	Ala	Lys	Gln	Asp	Ala	Tyr	Trp	Ala	
181				330					335					340			
182	cac	cac	gac	ctg	tat	ctg	ctg	gct	tat	gcg	ctg	tgg	ccg	acc	ggc	ttc	2551
183	His	His	Asp	Leu	Tyr	Leu	Leu	Ala	Tyr	Ala	Leu	Trp	Pro	Thr	Gly	Phe	
184			345					350					355				
185	ttc	cgt	ctg	gcg	ctg	ccg	gat	cag	gaa	gaa	atg	gag	tgg	ttc	gag	gcc	2599
186	Phe	Arg	Leu	Ala	Leu	Pro	Asp	Gln	Glu	Glu	Met	Glu	Trp	Phe	Glu	Ala	
187		360					365					370					
188	aac	tac	ccc	ggc	tgg	tac	gac	cac	tac	ggc	aag	atc	tac	gag	gaa	tgg	2647
189	Asn	Tyr	Pro	Gly	Trp	Tyr	Asp	His	Tyr	Gly	Lys	Ile	Tyr	Glu	Glu	Trp	
190	375					380					385					390	
191	cgc	gcc	cgc	ggg	tgc	gag	gat	ccg	tcc	tcg	ggc	ttc	atc	ccg	ctg	atg	2695
192	Arg	Ala	Arg	Gly	Cys	Glu	Asp	Pro	Ser	Ser	Gly	Phe	Ile	Pro	Leu	Met	
193				395						400					405		
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195	Trp	Phe	Ile	Glu	Asn	Asn	His	Pro	Ile	Tyr	Ile	Asp	Arg	Val	Ser	Gln	
196			410					415					420				
197	gtg	ccg	ttc	tgc	ccg	agc	ttg	gcc	aag	ggc	gcc	agc	acc	ctg	cgc	gtg	2791
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199			425					430					435				
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201	His	Glu	Tyr	Asn	Gly	Glu	Met	His	Thr	Phe	Ser	Asp	Gln	Trp	Gly	Glu	
202		440					445					450					
203	cgc	atg	tgg	ctg	gcc	gag	ccg	gag	cgc	tac	gag	tgc	cag	aac	atc	ttc	2887
204	Arg	Met	Trp	Leu	Ala	Glu	Pro	Glu	Arg	Tyr	Glu	Cys	Gln	Asn	Ile	Phe	
205	455					460					465					470	
206	gaa	cag	tac	gaa	gga	cgc	gaa	ctg	tcg	gaa	gtg	atc	gcc	gaa	ctg	cac	2935
207	Glu	Gln	Tyr	Glu	Gly	Arg	Glu	Leu	Ser	Glu	Val	Ile	Ala	Glu	Leu	His	
208				475						480					485		
209	ggg	ctg	cgc	agt	gat	ggc	aag	acc	ctg	atc	gcc	cag	ccg	cat	gtc	cgt	2983
210	Gly	Leu	Arg	Ser	Asp	Gly	Lys	Thr	Leu	Ile	Ala	Gln	Pro	His	Val	Arg	
211			490						495					500			
212	ggc	gac	aag	ctg	tgg	acg	ttg	gac	gat	atc	aaa	cgc	ctg	aac	tgc	gtc	3031
213	Gly	Asp	Lys	Leu	Trp	Thr	Leu	Asp	Asp	Ile	Lys	Arg	Leu	Asn	Cys	Val	
214			505					510					515				
215	ttc	aag	aac	ccg	gtg	aag	gca	ttc	aat	tga	aacgggtg	gtc	gggctccg	gtc			3081

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219 atg agc atg tta gga gaa aga cgc cgc ggt ctg acc gat ccg gaa atg 3189
220 Met Ser Met Leu Gly Glu Arg Arg Arg Gly Leu Thr Asp Pro Glu Met
W--> 221 1      5      10      15
222 gcg gcc gtc att ttg aag gcg ctt cct gaa gct ccg ctg gac ggc aac 3237
223 Ala Ala Val Ile Leu Lys Ala Leu Pro Glu Ala Pro Leu Asp Gly Asn
224      20      25      30
225 aac aag atg ggt tat ttc gtc acc ccc cgc tgg aaa cgc ttg acg gaa 3285
226 Asn Lys Met Gly Tyr Phe Val Thr Pro Arg Trp Lys Arg Leu Thr Glu
227      35      40      45
228 tat gaa gcc ctg acc gtt tat gcg cag ccc aac gcc gac tgg atc gcc 3333
229 Tyr Glu Ala Leu Thr Val Tyr Ala Gln Pro Asn Ala Asp Trp Ile Ala
230      50      55      60
231 ggc ggc ctg gac tgg ggc gac tgg acc cag aaa ttc cac ggc ggc cgc 3381
232 Gly Gly Leu Asp Trp Gly Asp Trp Thr Gln Lys Phe His Gly Gly Arg
233 65      70      75      80
234 cct tcc tgg ggc aac gag acc acg gag ctg cgc acc gtc gac tgg ttc 3429
235 Pro Ser Trp Gly Asn Glu Thr Thr Glu Leu Arg Thr Val Asp Trp Phe
236      85      90      95
237 aag cac cgt gac ccg ctc cgc cgt tgg cat gcg ccg tac gtc aag gac 3477
238 Lys His Arg Asp Pro Leu Arg Arg Trp His Ala Pro Tyr Val Lys Asp
239      100      105      110
240 aag gcc gag gaa tgg cgc tac acc gag cgc ttc ctg cag ggt tac tcc 3525
241 Lys Ala Glu Trp Arg Tyr Thr Asp Arg Phe Leu Gln Gly Tyr Ser
242      115      120      125
243 gcc gac ggt cag atc cgg gcg atg aac ccg acc tgg cgg gac gag ttc 3573
244 Ala Asp Gly Gln Ile Arg Ala Met Asn Pro Thr Trp Arg Asp Glu Phe
245      130      135      140
246 atc aac cgg tat tgg ggc gcc ttc ctg ttc aac gaa tac gga ttg ttc 3621
247 Ile Asn Arg Tyr Trp Gly Ala Phe Leu Phe Asn Glu Tyr Gly Leu Phe
248 145      150      155      160
249 aac gct cat tcg cag ggc gcc cgg gag gcg ctg tcg gac gta acc cgc 3669
250 Asn Ala His Ser Gln Gly Ala Arg Glu Ala Leu Ser Asp Val Thr Arg
251      165      170      175
252 gtc agc ctg gct ttc tgg ggc ttc gac aag atc gac atc gcc cag atg 3717
253 Val Ser Leu Ala Phe Trp Gly Phe Asp Lys Ile Asp Ile Ala Gln Met
254      180      185      190
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256 Ile Gln Leu Glu Arg Gly Phe Leu Ala Lys Ile Val Pro Gly Phe Asp
257      195      200      205
258 gag tcc aca gcg gtg ccg aag gcc gaa tgg acg aac ggg gag gtc tac 3813
259 Glu Ser Thr Ala Val Pro Lys Ala Glu Trp Thr Asn Gly Glu Val Tyr
260      210      215      220
261 aag agc gcc cgt ctg gcc gtg gaa ggg ctg tgg cag gag gtg ttc gac 3861
262 Lys Ser Ala Arg Leu Ala Val Glu Gly Leu Trp Gln Glu Val Phe Asp
263 225      230      235      240
264 tgg aac gag agc gct ttc tcg gtg cac gcc gtc tat gac gcg ctg ttc 3909

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:293 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
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L:436 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:439 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5
L:442 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5